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<110> Bayer CropScience GmbH

<120> Plants with increased activity of a Class 3 branching enzyme

<130> BCS 03-5005-PCT

<150> EP 03090324.9

<151> 2003-09-30

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<170> PatentIn version 3.1

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WO 2005/030941 FC 1/EF

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cag ctt aa Gln Leu Ly	a ttt gtt s Phe Val 35	cgc agc Arg Ser	cgc cgg Arg Arg 40	gct c Ala A	ga gtt Arg Val	tcg agg Ser Arg 45	tgt Cys	aga Arg	145
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cgt gaa ag Arg Glu Ar	a tat aa g Tyr Ly: 10	s Ser Lei	aag gae Lys As	ttg applementation to the control of	aag gat Lys Asp	gaa ata Glu Ile	ttg Leu 110	act Thr	337
cgt cat tt Arg His Ph	c agt cto le Ser Le 115	c aag gag u Lys Gli	y atg tc Wet Se 12	r Inr	ggg tat Gly Tyr	gaa tta Glu Leu 125	мет	ggt Gly	385
atg cat co Met His At 13	gc aac at ng Asn Il 80	a caa cat e Gln His	cga gt Arg Va 135	g gat T Asp	ttc ttg Phe Leu	gaa tgg Glu Trp 140	gct Ala	cca Pro	433
ggt gct co Gly Ala Ai 145	rg Tyr Cy	s Ala Lei 15) Tie Gi	у АЅР	155	GIY IT	ser.	1111	481
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tat tgg t Tyr Trp P	tt att at ne Ile Il 18	e Leu Gi	a gat aa u Asp Ly	tta s Leu 185	cgt gaa Arg Glu	ı gga gaa ı Gly Glı	gaa Glu 190	cct Pro	577
gat aaa t Asp Lys L	eu Tyr Ph 195	ie Gin Gi	n Tyr As 20	on Tyr	Ala GIL	20	r Giy	Lys	625
ggt gac a Gly Asp T 2	cg ggt at hr Gly I 10	t acc gt le Thr Va	c gag ga 1 Glu G 215	aa atc lu Ile	ttt aaa Phe Lys	a aaa gc s Lys Ala 220	a aat a Asn	gat Asp	673
gag tat t Glu Tyr T 225	gg gaa ce rp Glu Pi	t gga ga ro Gly Gl 23	u ASP A	gc ttc rg Phe	att aaa Ile Ly: 23	s Ser Ar	t tat g Tyr	gag Glu	721
gtg gca g Val Ala A 240	ca aag t [.] la Lys Lo	ta tat ga eu Tyr Gl 245	ug gaa a' u Glu M	tg ttc et Phe	gga cca Gly Pro 250	a aat gg o Asn Gl	a cct y Pro	caa Gln 255	769

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act Thr	tgg Trp	aaa Lys	gag Glu 275	caa Gln	caa Gln	aaa Lys	gag Glu	gat Asp 280	ccg Pro	gca Ala	agc Ser	aat Asn	ttg Leu 285	cca Pro	tcg Ser	865
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cca Pro	atg Met	tca Ser	a ago Ser 759	Asr	aat Asr	tto Phe	tco Sei	r Phe 760	e Sei	t ctg	g gct I Ala	: aac I Asr	cgt Arg 765	arg	tgg Trp	2305
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Met Pro Ala Leu Pro His Gly Ser Lys Tyr Arg Val Tyr Phe Asn Thr 340 345 350 Pro Asn Gly Pro Leu Glu Arg Val Pro Ala Trp Ala Asn Phe Val Ile 355 360 365 Pro Asp Ala Gly Gly Met Ala Leu Ala Val His Trp Glu Pro Pro 370 380 Glu Tyr Ala Tyr Lys Trp Lys His Lys Leu Pro Val Lys Pro Lys Ser 385 390 395 Leu Arg Ile Tyr Glu Cys His Val Gly Ile Ser Gly Gln Glu Pro Lys 405 410 415 Val Ser Ser Phe Asn Asp Phe Ile Ser Lys Val Leu Pro His Val Lys 420 425 430 Glu Ala Gly Tyr Asn Ala Ile Gln Ile Ile Gly Val Val Glu His Lys 435 440 445 Asp Tyr Phe Thr Val Gly Tyr Arg Val Thr Asn Phe Tyr Ala Val Ser 450 455 460 Ser Arg Tyr Gly Thr Pro Asp Asp Phe Lys Arg Leu Val Asp Glu Ala 465 470 475 480 His Gly Leu Gly Leu Leu Val Phe Leu Glu Ile Val His Ser Tyr Ala 485 490 495 Ala Ala Asp Glu Met Val Gly Leu Ser Leu Phe Asp Gly Ala Asn Asp 500 510 Cys Tyr Phe His Thr Gly Lys Arg Gly His His Lys Phe Trp Gly Thr 515 520 525 Arg Met Phe Lys Tyr Gly Asp Leu Asp Val Leu His Phe Leu Leu Ser 530 535 540 Asn Leu Asn Trp Trp Val Glu Glu Tyr His Val Asp Gly Phe His Phe 545 550 550 His Ser Leu Ser Ser Met Leu Tyr Thr His Asn Gly Phe Ala Ser Phe 565 570 Thr Gly Asp Met Asp Glu Tyr Cys Asn Gln Tyr Val Asp Lys Glu Ala 580 585 Leu Leu Tyr Leu Ile Leu Ala Asn Glu Val Leu His Ala Leu His Pro 600 605

Asn Val Ile Thr Ile Ala Glu Asp Ala Thr Leu Tyr Pro Gly Leu Cys 610 620 Asp Pro Thr Ser Gln Gly Gly Leu Gly Phe Asp Tyr Phe Ala Asn Leu 625 630 635 Ser Ala Ser Glu Met Trp Leu Ala Leu Leu Glu Asn Thr Pro Asp His 645 650 655 Glu Trp Cys Met Ser Lys Ile Val Ser Thr Leu Val Gly Asp Arg Gln
660 665 670 Asn Thr Asp Lys Met Leu Leu Tyr Ala Glu Asn His Asn Gln Ser Ile 675 685 Ser Gly Gly Arg Ser Phe Ala Glu Ile Leu Ile Gly Asn Ser Leu Gly 690 700 Lys Ser Ser Ile Ser Gln Glu Ser Leu Leu Arg Gly Cys Ser Leu His 705 710 715 720 Lys Met Ile Arg Leu Ile Thr Ser Thr Ile Gly Gly His Ala Tyr Leu 725 730 735 Asn Phe Met Gly Asn Glu Phe Gly His Pro Lys Arg Val Glu Phe Pro 740 745 750 Met Ser Ser Asn Asn Phe Ser Phe Ser Leu Ala Asn Arg Arg Trp Asp 755 760 765 Leu Leu Glu Asp Val Val His Tyr Gln Leu Phe Ser Phe Asp Lys Gly 770 780 Met Met Asp Leu Asp Lys Asn Gly Arg Ile Leu Ser Arg Gly Leu Ala 785 790 795 800 Asn Ile His His Val Asn Asp Thr Thr Met Val Ile Ser Tyr Leu Arg 805 810 815 Gly Pro Asn Leu Phe Val Phe Asn Phe His Pro Val Asn Ser Tyr Glu 820 825 830 Arg Tyr Ile Ile Gly Val Glu Glu Ala Gly Glu Tyr Gln Val Thr Leu 835 840 845 Asn Thr Asp Glu Asn Lys Tyr Gly Gly Arg Gly Leu Leu Gly His Asp 850 855 860 Gln Asn Ile Gln Arg Thr Ile Ser Arg Arg Ala Asp Gly Met Arg Phe 865 870 875 880

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Cys Leu Glu Val Pro Leu Pro Ser Arg Ser Ala Gln Val Tyr Lys Leu 885 890 895

Thr Arg Ile Leu Arg Ala 900